

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2005, 16:37:09 ; Search time 7.16981 Seconds
(without alignments)
203.901 Million cell updates/sec

Title: US-10-074-694-5

Perfect score: 803
Sequence: 1 MANLERTFAIKPDGVQRL.....WFKPELVYKSCAHDWYE 152

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 57320 seqs, 9617956 residues

Total number of hits satisfying chosen parameters: 57320

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA New:
1: /cgn2_6/prodata/1/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/prodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/prodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/prodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/prodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/prodata/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/prodata/1/paa/US11_NEW_COMB.pep.*
8: /cgn2_6/prodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 16, 2005, 16:32:00 (without alignments)
534.625 Million cell updates/sec

Title: US-10-074-694-5
Perfect score: 803
Sequence: 1 MANLEPFAIKPDGVORGL.....WFKPELVYKSCAHNVE 152

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues
Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Parents AA Main:

1: /cgn2_6/prodata/1/paa/US066_COMB.pep.*
2: /cgn2_6/prodata/1/paa/US073_COMB.pep.*
3: /cgn2_6/prodata/1/paa/US074_COMB.pep.*
4: /cgn2_6/prodata/1/paa/US075_COMB.pep.*
5: /cgn2_6/prodata/1/paa/US076_COMB.pep.*
6: /cgn2_6/prodata/1/paa/US077_COMB.pep.*
7: /cgn2_6/prodata/1/paa/US078_COMB.pep.*
8: /cgn2_6/prodata/1/paa/US079_COMB.pep.*
9: /cgn2_6/prodata/1/paa/US080_COMB.pep.*
10: /cgn2_6/prodata/1/paa/US081_COMB.pep.*
11: /cgn2_6/prodata/1/paa/US082_COMB.pep.*
12: /cgn2_6/prodata/1/paa/US083_COMB.pep.*
13: /cgn2_6/prodata/1/paa/US084_COMB.pep.*
14: /cgn2_6/prodata/1/paa/US085_COMB.pep.*
15: /cgn2_6/prodata/1/paa/US086_COMB.pep.*
16: /cgn2_6/prodata/1/paa/US087_COMB.pep.*
17: /cgn2_6/prodata/1/paa/US088_COMB.pep.*
18: /cgn2_6/prodata/1/paa/US089_COMB.pep.*
19: /cgn2_6/prodata/1/paa/US090_COMB.pep.*
20: /cgn2_6/prodata/1/paa/US091_COMB.pep.*
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22: /cgn2_6/prodata/1/paa/US093_COMB.pep.*
23: /cgn2_6/prodata/1/paa/US094_COMB.pep.*
24: /cgn2_6/prodata/1/paa/US095_COMB.pep.*
25: /cgn2_6/prodata/1/paa/US096_COMB.pep.*
26: /cgn2_6/prodata/1/paa/US097_COMB.pep.*
27: /cgn2_6/prodata/1/paa/US098_COMB.pep.*
28: /cgn2_6/prodata/1/paa/US099_COMB.pep.*
29: /cgn2_6/prodata/1/paa/US100_COMB.pep.*
30: /cgn2_6/prodata/1/paa/US101_COMB.pep.*
31: /cgn2_6/prodata/1/paa/US102_COMB.pep.*
32: /cgn2_6/prodata/1/paa/US103_COMB.pep.*
33: /cgn2_6/prodata/1/paa/US104_COMB.pep.*
34: /cgn2_6/prodata/1/paa/US105_COMB.pep.*
35: /cgn2_6/prodata/1/paa/US106_COMB.pep.*
36: /cgn2_6/prodata/1/paa/US107_COMB.pep.*
37: /cgn2_6/prodata/1/paa/US108_COMB.pep.*
38: /cgn2_6/prodata/1/paa/US109_COMB.pep.*
39: /cgn2_6/prodata/1/paa/US110_COMB.pep.*
40: /cgn2_6/prodata/1/paa/US111_COMB.pep.*
41: /cgn2_6/prodata/1/paa/US112_COMB.pep.*
42: /cgn2_6/prodata/1/paa/US114_COMB.pep.*
43: /cgn2_6/prodata/1/paa/US114_COMB.pep.*

44: /cgn2_6/prodata/1/paa/US600_COMB.pep.*
45: /cgn2_6/prodata/1/paa/US601_COMB.pep.*
46: /cgn2_6/prodata/1/paa/US602_COMB.pep.*
47: /cgn2_6/prodata/1/paa/US603_COMB.pep.*
48: /cgn2_6/prodata/1/paa/US604_COMB.pep.*
49: /cgn2_6/prodata/1/paa/US605_COMB.pep.*
50: /cgn2_6/prodata/1/paa/US606_COMB.pep.*
51: /cgn2_6/prodata/1/paa/US607_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES